\_\_\_\_\_\_

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=4; day=15; hr=15; min=37; sec=0; ms=546; ]

\_\_\_\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*

Reviewer Comments:

<160> 26

The number provided for numeric identifier <160> must match the total number of sequences in the file. There were 28 sequences counted in this sequence listing. Numeric identifier <160> states there are a total of 26 sequences. Please make all necessary changes.

<210> 27

<211> 20

<212> DNA

<213> homo sapien

<400> 27

atcgacaagg tacccaggat

The sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." The enumeration is not marked in the right margin for SEQ ID # 27 and 28, please make all necessary changes.

Numeric Identifier <213> response should be corrected the first letter should be upper case as below:

<213> Homo Sapien

To correct the sequence listing errors noted in this report - The recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in Patent In, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

# Validated By CRFValidator v 1.0.3

Application No: 10574182 Version No: 2.0

Input Set:

Output Set:

**Started:** 2011-04-06 19:48:13.071

Finished: 2011-04-06 19:48:15.124

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 53 ms

Total Warnings: 28

Total Errors: 3

No. of SeqIDs Defined: 26

Actual SeqID Count: 28

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (1)
W	402	Undefined organism found in <213> in SEQ ID (2)
W	402	Undefined organism found in <213> in SEQ ID (3)
W	402	Undefined organism found in <213> in SEQ ID (4)
W	402	Undefined organism found in <213> in SEQ ID (5)
W	402	Undefined organism found in <213> in SEQ ID (6)
W	402	Undefined organism found in <213> in SEQ ID (7)
W	402	Undefined organism found in <213> in SEQ ID (8)
W	402	Undefined organism found in <213> in SEQ ID (9)
W	402	Undefined organism found in <213> in SEQ ID (10)
W	402	Undefined organism found in <213> in SEQ ID (11)
W	402	Undefined organism found in <213> in SEQ ID (12)
W	402	Undefined organism found in <213> in SEQ ID (13)
W	402	Undefined organism found in <213> in SEQ ID (14)
W	402	Undefined organism found in <213> in SEQ ID (15)
W	402	Undefined organism found in <213> in SEQ ID (16)
W	402	Undefined organism found in <213> in SEQ ID (17)
W	402	Undefined organism found in <213> in SEQ ID (18)
W	402	Undefined organism found in <213> in SEQ ID (19)
W	402	Undefined organism found in <213> in SEQ ID (20)

### Input Set:

# Output Set:

**Started:** 2011-04-06 19:48:13.071 **Finished:** 2011-04-06 19:48:15.124

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 53 ms

Total Warnings: 28

Total Errors: 3

No. of SeqIDs Defined: 26

Actual SeqID Count: 28

Error code		Error Description
		This error has occured more than 20 times, will not be displayed
E	254	The total number of bases conflicts with running total Input: 0, Calculated: 20 SEQID(27)
E	254	The total number of bases conflicts with running total Input: 0, Calculated: 20 SEQID(28)
E	252	Calc# of Seq. differs from actual; 26 seqIds defined; count=28

### SEQUENCE LISTING

```
<110> Albert, Lai
<120> NOVEL SPLICE VARIANTS OF HUMAN Dkkl1
<130> PP023359.0003
<140> 10574182
<141> 2011-04-06
<150> PCT/US04/34256
<151> 2004-09-30
<150> 60/507682
<151> 2003-09-30
<160> 26
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 819
<212> DNA
<213> homo sapien
<400> 1
atgggagaag cctccccacc tgcccccgca aggcggcatc tgctggtcct gctgctgctc 60
ctctctaccc tggtgatccc ctccgctgca gctcctatcc atgatgctga cgcccaagag 120
agctccttgg gtctcacagg cctccagagc ctactccaag gcttcagccg acttttcctg 180
aaaggtaacc tgcttcgggg catagacagc ttattctctg cccccatgga cttccggggc 240
ctccctggga actaccacaa agaggagaac caggagcacc agctggggaa caacaccctc 300
tccagccacc tccagatcga caagaggacc gacaacaaga caggagaggt gctgatctcc 360
gagaatgtgg tggcatccat tcaaccagcg gaggggagct tcgagggtga tttgaaggta 420
cccaggatgg aggagaagga ggccctggta cccatccaga aggccacgga cagcttccac 480
acagaactcc atccccgggt ggccttctgg atcattaagc tgccacggcg gaggtcccac 540
caggatgccc tggagggcgg ccactggctc agcgagaagc gacaccgcct gcaggccatc 600
cgggatggac tccgcaaggg gacccacaag gacgtcctag aagaggggac cgagagctcc 660
teccaeteca ggetgteece eegaaagaee eacttaetgt acateeteag geeetetegg 720
cagetgtagg ggtggggace ggggagcace tgcetgtage ecceateaga ecetgeecea 780
agcaccatat ggaaataaag ttctttctta catctaaca
                                                                  819
<210> 2
<211> 242
<212> PRT
<213> homo sapien
<400> 2
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1
                 5
                                    10
Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Pro
                                25
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
```

40

45

35

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 5.5 60 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 7.0 75 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly 8.5 90 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Arg Thr Asp Asn 100 105 110 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 120 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu 135 140 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His 150 155 Thr Glu Leu His Pro Arq Val Ala Phe Trp Ile Ile Lys Leu Pro Arq 165 170 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu 185 180 190 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr 200 His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser His Ser Arg 215 220 Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg 225 230 235 240 Gln Leu

<210> 3 <211> 733 <212> DNA <213> homo sapien

#### <400> 3

caccatgga gaageetece cacetgeeee egeaaggegg catetgetgg teetgetget 60 geteetetet accetggtga teeceteege tgeageteet atecatgatg etgaegeeea 120 agagagetee ttgggtetea caggeeteea gageetacte caaggettea geegaetttt 180 cetgaaaggt aacetgette ggggeataga cagettatte tetgeeeeea tggaetteeg 240 gggeeteeet gggaactace acaagagga gaaceaggag caccagetgg ggaacaacac 300 cetetecage caceteeaga tegacaagat gacegacaac aagacaggag aggtgetgat 360 ctcegagaat gtggtggeat ecattecaace ageggagggg agettegagg gtgatttgaa 420 ggtaeceagg atggaggaa aggaggeeet ggtaeceate cagaaggeea eggaegget 480 ccacacagaa etceateeee gggtggeett etggateatt aagetgeeae ggeggaggte 540 ccaccaggat geeetggagg geggeeaetg getaeggag aagegaeaee geetgeagge 600 cateeggat geaeteega aggggaeeea caaggaegte etagaagagg ggaeegaaga 660 cteeteeeae teeaggetg eceeegaaa gaeecaactta etgtaeatee teaggeeete 720 teggeagetg tag

<210> 4 <211> 242 <212> PRT <213> homo sapien

<400> 4

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val 1 5 10 15 15 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro

2.0 2.5

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu 40 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 55 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 70 75 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly 90 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn 100 105 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 115 120 125 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu 135 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His 155 150 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg 165 170 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu 185 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr 200 His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser His Ser Arg 215 Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg 225 230 235 240 Gln Leu

<210> 5 <211> 733 <212> DNA <213> homo sapien

<400> 5

caccatggga gaagecteec cacctgeece egcaaggegg catctgetgg teetgetget 60 getectetet accetggtga teccetecae tgeageteet atecatgatg etgacgeeca 120 agagagetee ttgggtetea caggeeteea gageetaete caaggettea geegaetttt 180 cctgaaaggt aacctgcttc ggggcataga cagcttattc tctgccccca tggacttccg 240 gggcctccct gggaactacc acaaagagga gaaccaggag caccagctgg ggaacaacac 300 cctctccagc cacctccaga tcgacaagat gaccgacaac aagacaggag aggtgctgat 360 ctccgagaat gtggtggcat ccattcaacc agcggagggg agcttcgagg gtgatttgaa 420 ggtacccagg atggaggaga aggaggccct ggtacccatc cagaaggcca cggacagctt 480 ccacacagaa ctccatcccc gggtggcctt ctggatcatt aagctgccac ggcggaggtc 540 ccaccaggat gccctggagg gcggccactg gctcagcgag aagcgacacc gcctgcaggc 600 catccgggat ggactccgca aggggaccca caaggacgtc ctagaagagg ggaccgagag 660 ctcctcccac tccaggctgt ccccccgaaa gacccactta ctgtacatcc tcaggccctc 720 733 tcggcagctg tag

<210> 6 <211> 242 <212> PRT <213> homo sapien Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val 1 5 10 Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Thr Ala Ala Pro 25 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu 40 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 55 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 70 75 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly 85 90 95 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn 105 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 120 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu 135 140 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His 150 155 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg 165 170 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu 180 185 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr 200 205 His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser His Ser Arg 215 220 Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg 230 235 Gln Leu

<210> 7

<211> 733

<212> DNA

<213> homo sapien

## <400> 7

caccatgga gaagcetece cacctgecee egeaaggegg catetgetgg teetgetget 60 getectetet accetggtga teecetecae tgeageteet atecatgatg etgaegeee 120 agagagetee ttgggtetea caggeeteea gageetaete caaggettea geegaetttt 180 cetgaaaggt aacetgette ggggeataga cagettatte tetgeeceea tggaetteeg 240 gggeeteeet gggaactaee acaagagga gaaceaggag caccagetgg ggaacaacae 300 cetetecage cacetecaga tegacaagat gaccgaacae aagacaggag aggtgetgat 360 cteegagaat gtggtggeat ecatteaace ageggagggg agettegagg gtgattgaa 420 ggtaeceagg atggaggaa aggaggeeet ggtaeceate cagaaggeea eggaegget 480 ceaccaggaa etceateeee gggtggeett etggateatt aagetgeeae ggeggaggte 540 ceaccaggat geeetggagg geggeeaetg geteagegg aagetgeaee geetgeagge 600 cateeggaa teeaggetg eceecegaaa gaeceaetta etgtaeatee teaggeete 720 teggeagetg tag

<210> 8

<211> 242

<212> PRT

<400> 8

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val 5 10 Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Thr Ala Ala Pro 20 25 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu 40 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 55 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 7.5 65 70 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly 90 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn 100 105 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 120 125 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu 135 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His 145 150 155 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg 165 170 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu 180 185 190 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr 200 His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser His Ser Arg 215 Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg 225 230 235 240 Gln Leu

<210> 9 <211> 733 <212> DNA

<213> homo sapien

<400> 9

caccatggga gaagcetece cacctgeece egeaaggegg catetgetgg teetgetget 60 geteetetet accetggtga teeceteeae tgeageteet atecatgatg etgaegeeca 120 agagagetee ttgggtetea caggeeteea gageetaete caaggettea geegaettt 180 cetgaaaggt aacetgette ggggeataga cagettatte tetgeeceea tggaetteeg 240 gggeeteeet gggaactaee acaagagga gaaceaggag caccagetgg ggaacaacae 300 cetetecage cacctecaga tegaeaagat gaecgaeaae aagaeaggag agettegag gtgattgaa 420 ggtaeceagg atggaggaa aggaggeeet ggtaeceate cagaaggeea eggaeageet 480 ceacacagaa etceateee gggtggeett etggateatt aagetgeeae ggeggaggte 540 ceaceaggat geeetggagg geageeet getaeceate aageegaeae geetgeagge 600 cateeggat geacteega aggggaecea caaggaegte etaaaagagg ggaecgaaga 660 cteeteeae tecaggetg tag 533

```
<212> PRT
<213> homo sapien
<400> 10
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1
                5
                                  10
Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Thr Ala Ala Pro
                              25
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
             40
                                             45
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
                      55
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
                  7.0
                                     7.5
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
                                  90
               8.5
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
                              105
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
                         120
                                             125
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
                                         140
                      135
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
                 150
                                    155
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
                                  170
               165
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Ser His Trp Leu Ser Glu
           180
                             185
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
                          200
                                              205
His Lys Asp Val Leu Lys Glu Gly Thr Glu Ser Ser His Ser Arg
                               220
                      215
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225
                 230
                                      235
                                                         240
Gln Leu
<210> 11
<211> 733
<212> DNA
<213> homo sapien
<400> 11
caccatggga gaagecteee cacctgeece egeaaggegg catetgetgg teetgetget 60
geteetetet accetggtga teccetecae tgeageteet atceatgatg etgaegeeca 120
agagagetee ttgggtetea eaggeeteea gageetaete eaaggettea geegaetttt 180
cctgaaaggt aacctgcttc ggggcataga cagcttattc tctgccccca tggacttccg 240
gggcctccct gggaactacc acaaagagga gaaccaggag caccagctgg ggaacaacac 300
cctctccagc cacctccaga tcgacaagat gaccgacaac aagacaggag aggtgctgat 360
ctccgagaat gtggtggcat ccattcaacc agcggagggg agcttcgagg gtgatttgaa 420
ggtacccagg atggaggaga aggaggccct ggtacccatc cagaaggcca cggacagctt 480
ccacacagaa ctccatcccc gggtggcctt ctggatcatt aagctgccac ggcggaggtc 540
ccaccaggat gccctggagg gcggccactg gctcagcgag aagcgacacc gcctgcaggc 600
```

catccgggat ggactccgca aggggaccca caaggacgtc ctagaagagg ggaccgagag 660

<210> 10 <211> 242 <210> 12 <211> 242 <212> PRT

<213> homo sapien

<400> 12

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val 1 5 10 15 Leu Leu Leu Pro Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Thr Ala Ala Pro

20 25 30

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu 35 40 45

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu 50 55 60

Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly 65 70 75 80

Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95

Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn 100 105 110

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln 115 120 125

Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu